



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> BioImage A/S  
Thastrup, Ole

<120> Novel Florescent Proteins

<130> 3759-0106P

<140> unknown

<141> 2001-06-01

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C<sup>2</sup>  
<170> PatentIn version 3.1

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<211> 764

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (8) .. (721)

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gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 35 40 45	145
att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 50 55 60	193
act ttc tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met 65 70 75	241
aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 80 85 90	289
gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 95 100 105 110	337
gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 115 120 125	385
ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu 130 135 140	433
tac aac tat aac tca cat aat gta tac atc atg gca gac aaa cca aag Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys 145 150 155	481
aat gga atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly 160 165 170	529
agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 175 180 185 190	577
ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 195 200 205	625
ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu 210 215 220	673
ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 225 230 235	721
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<213> Aequorea victoria

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val  
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
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<210> 3

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<212> DNA

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<222> (1)..(717)

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20 25 30	

ggg gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	

tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag	240
Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc 336  
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att 384  
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat 432  
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
130 135 140

tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc 480  
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
145 150 155 160

atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga agc gtt 528  
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
165 170 175

caa tta gca gac cat tat caa caa aat act cca att ggc gat ggc cct 576  
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc ctt tcc 624  
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta 672  
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val  
210 215 220

aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa taa 717  
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
225 230 235

atgtccagac ttccaattga cactaaaggg atccgaattc 757

<210> 4

<211> 238

<212> PRT

<213> Aequorea victoria

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Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35					40					45			
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
	50					55					60				
Ser	His	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
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His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100					105						110	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met	Glu	Tyr	Asn
	130					135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys	Asn	Gly
145					150					155					160
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly	Ser	Val
			165						170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		195					200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu	Glu	Phe	Val
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<222> (1)..(777)

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gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt gga gag 96  
Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag 240  
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc 336  
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att 384  
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat 432  
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn

130	135	140	
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly			
145	150	155	160
atg gaa tac aat tat aac tca cat aat gta tac atc atg gca gac aaa			528
Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys			
	165	170	175
cca aag aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa			576
Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys			
	180	185	190
gat gga agc gtt caa tta gca gac cat tat caa caa aat act cca att			624
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile			
	195	200	205
ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa			672
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln			
	210	215	220
tct gcc ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt			720
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu			
	225	230	235
ctt gag ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta			768
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu			
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<212> PRT

<213> Aequorea victoria

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20 25 30

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35 40 45



Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
145 150 155 160

Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys  
165 170 175

Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys  
180 185 190

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
195 200 205

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln  
210 215 220

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu  
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Tyr Lys

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gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt gga gag 96  
Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

act tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag 240  
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc 336  
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att 384  
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat 432  
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
130 135 140

tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc 480  
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
145 150 155 160

atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga agc gtt 528  
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
165 170 175

caa tta gca gac cat tat caa caa aat act cca att ggc gat ggc cct 576  
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc ctt tcc 624  
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta 672  
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val  
210 215 220

aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa taa 717  
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
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atgtccagac ttccaattga cactaaaggg atccgaattc 757

<210> 8

<211> 238

<212> PRT

<213> Aequorea victoria

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
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Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln

C2  
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70

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80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
165 170 175

C21 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val  
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
225 230 235

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